

SEQUENCE LISTING

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<120> HYBRID CARRIERS FOR NUCLEIC ACID CARGO

<130> CRV16P02PC2 - CV146 - P231

<160> 19

<170> PatentIn version 3.5

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<212> RNA

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<223> formula_V

$\langle 400 \rangle$ 1

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<223> formula_V

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auccgagucg cauacuacgg uacuggugac agaccuaggu cgucaguuga ccaguccgcc	180
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ccucuagagc uacgcagguu cgcauuaaaa gcguugauua gugugcauag aacagaccuc	600
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auccacagcu gaugaaagac uugugcgguu cgguuuauu cccuuuuuuu uuuuuuuuuu	180
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auccacagcu gaugaaagac uugugcggua cgguuaaucu cccuuuuuuu uuuuuuuuuu 180
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 <223> formula_VI

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<212> PRT
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<220>
<223> GpLuc amino acid sequence

<400> 11

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Ser Asn Phe Ala Thr Thr Asp Leu Asp Ala Asp Arg Gly Lys Leu Pro
35 40 45

Gly Lys Lys Leu Pro Leu Glu Val Leu Lys Glu Met Glu Ala Asn Ala
50 55 60

Arg Lys Ala Gly Cys Thr Arg Gly Cys Leu Ile Cys Leu Ser His Ile
65 70 75 80

Lys Cys Thr Pro Lys Met Lys Lys Phe Ile Pro Gly Arg Cys His Thr
85 90 95

Tyr Glu Gly Asp Lys Glu Ser Ala Gln Gly Gly Ile Gly Glu Ala Ile
100 105 110

Val Asp Ile Pro Glu Ile Pro Gly Phe Lys Asp Leu Glu Pro Met Glu
115 120 125

Gln Phe Ile Ala Gln Val Asp Leu Cys Val Asp Cys Thr Thr Gly Cys
130 135 140

Leu Lys Gly Leu Ala Asn Val Gln Cys Ser Asp Leu Leu Lys Lys Trp
 145 150 155 160

Leu Pro Gln Arg Cys Ala Thr Phe Ala Ser Lys Ile Gln Gly Gln Val
 165 170 175

Asp Lys Ile Lys Gly Ala Gly Gly Asp
 180 185

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 cccccaagau gaagaaguuc auccccgggc gcugccacac cuacgagggc gacaaggaga 360
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 ggggcgacug aggacuagug caucacauuu aaaagcaucu cagccuacca ugagaauaag 660
 agaaaagaaaa ugaagaucua uagcuuuuuc aucucuuuuu cuuuuucguu gguguaaagc 720
 caacaccucg ucuaaaaaac auaaaauuuc uuaaucauuu ugccucuuuu cucugugcuu 780
 caauuaauaa aaaauggaaa gaaccuagau cuaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaugca uccccccccc cccccccccc 900

ccccccccc ccaaaggcuc uuucagagc caccagaauu 940

<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-UTR of human ribosomal protein Large 32 lacking the 5' terminal oligopyrimidine tract

<400> 13

ggcgctgcct acggaggtgg cagccatctc cttctcggca tc 42

<210> 14

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-UTR of ATP5A1 lacking the 5' terminal oligopyrimidine tract

<400> 14

gcggctcggc cattttgtcc cagtcagtcc ggaggctgcg gctgcagaag taccgcctgc 60

ggagtaactg caaag 75

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> histone stem-loop sequence

<400> 15

caaaggctct tttcagagcc acca 24

<210> 16

<211> 24

<212> RNA

<213> Artificial Sequence

<220>
<223> histone stem-loop sequence

<400> 16
caaaggcucu uuucagagcc acca

24

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<212> RNA
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<223> HA-R2564 mRNA

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ccgaccagca gagccuguac cagaacgccg acgccuacgu guucgugggc uccagccgcu 720
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aagagaaaga aaaugaagau caauagcuua uucaucucu uuucuuuuuc guugguguua	1860
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cuucaauuaa uaaaaaaaaugg aaagaaccua gaucuaaaaaa aaaaaaaaaa aaaaaaaaaa	1980
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 <223> Ppluc amino acid sequence

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20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp

210

215

220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
 225 230 235 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
 245 250 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
 260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
 275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
 290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
 305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
 325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
 340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
 355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
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Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
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Gly Gly Lys Ile Ala Val
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<211> 2035
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<220>
<223> Ppluc mRNA

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uaccaugaga	auaagagaaa	gaaaaugaag	aucaauagcu	uauucaucuc	uuuuucuuuu	1800
ucguuggugu	aaagccaaca	cccugucuaa	aaaacauaaa	uuucuuuaau	cauuuugccu	1860
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